

AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions, and listings, of claims in the application:

LISTING OF CLAIMS:

Claim 1. (Original) A method for increasing cellulose biosynthesis in cotton plants, comprising the step of:

providing cells of said cotton plant with a chimeric gene comprising the following operably linked DNA fragments

- i) a promoter expressible in said cell of said plant;
 - ii) a DNA region coding for the protein comprising the amino acid sequence of SEQ ID No. 5 or SEQ ID No 6 or SEQ ID No 7 or SEQ ID No 8 or a variant thereof, said variant having the same enzymatic activity;
 - iii) a 3' region involved in transcription termination and polyadenylation;
- thereby increasing cellulose biosynthesis in said plant.

Claim 2. (Original) The method of claim 1, wherein said DNA region comprises the nucleotide sequence of SEQ ID No 1 from the nucleotide at position 121 to the nucleotide at position 1986, or SEQ ID No. 2 from the nucleotide at position 47 to the nucleotide at position 1906, or SEQ ID No 3 or SEQ ID No 4 from the nucleotide at position 2 to the nucleotide at position 1576, or SEQ ID No. 9.

Claim 3. (Original) The method of claim 1, wherein said promoter is a constitutive promoter.

Claim 4. (Original) The method of claim 1, wherein said promoter is a fiber-specific promoter.

Claim 5. (Original) The method of claim 1, wherein said promoter is an expansin promoter.

Claim 6. (Original) The method of claim 1, wherein said cellulose biosynthesis is increased in lint fibers.

Claim 7. (Original) A method for decreasing cellulose biosynthesis in cotton plants comprising the step of:

providing cells of said cotton plant with a chimeric gene capable of reducing the expression of a gene endogenous to said cotton plant, wherein said endogenous gene codes for a protein comprising the amino acid sequence of SEQ ID No. 5 or SEQ ID No 6 or SEQ ID No 7 or SEQ ID No 8

thereby decreasing cellulose biosynthesis.

Claim 8. (Original) The method of claim 7, wherein said chimeric gene comprises 21 contiguous nucleotides selected from a nucleotide sequence which codes for a protein comprising the amino acid sequence of SEQ ID No. 5 or SEQ ID No 6 or SEQ ID No 7 or SEQ ID No 8,

operably linked to a plant expressible promoter and a 3' region involved in transcription termination and polyadenylation.

Claim 9. (Original) The method of claim 8, wherein said 21 contiguous nucleotides are selected from the nucleotide sequence of SEQ ID No 1 or SEQ ID No. 2 or SEQ ID No 3 or SEQ ID No 4 or SEQ ID No. 9.

Claim 10. (Original) The method of claim 7, wherein said chimeric gene comprises 21 contiguous nucleotides selected from the complement of a nucleotide sequence which codes for a protein comprising the amino acid sequence of SEQ ID No. 5 or SEQ ID No. 6 or SEQ ID No. 7 or SEQ ID No. 8,

operably linked to a plant expressible promoter and a 3' region involved in transcription termination and polyadenylation.

Claim 11. (Original) The method of claim 10, wherein said 21 contiguous nucleotides are selected from the complement of the nucleotide sequence of SEQ ID No. 1 or SEQ ID No. 2 or SEQ ID No. 3 or SEQ ID No. 4 or SEQ ID No. 9.

Claim 12. (Original) The method of claim 7, wherein said chimeric gene comprises a first nucleotide sequence of 21 contiguous nucleotides selected from a nucleotide sequence which codes for a protein comprising the amino acid sequence of SEQ ID No. 5 or SEQ ID No. 6 or SEQ ID No. 7 or SEQ ID No. 8, and

a second nucleotide sequence complementary to said first nucleotide sequence, operably linked to a plant-expressible promoter and a 3' region involved in transcription termination and polyadenylation

such that upon transcription of said chimeric gene, an RNA is formed which can form a double stranded RNA region between said first and said second nucleotide sequence.

Claim 13. (Original) The method of claim 12, wherein said 21 contiguous nucleotides are selected from the nucleotide sequence of SEQ ID No. 1 or SEQ ID No. 2 or SEQ ID No. 3 or SEQ ID No. 4 or SEQ ID No. 9.

Claim 14. (Original) The method of claim 7, wherein said plant expressible promoter is a constitutive promoter.

Claim 15. (Original) The method of claim 7, wherein said plant expressible promoter is a fuzz fiber specific promoter.

Claim 16. (Original) The method of claim 7, wherein said cellulose biosynthesis is decreased in fuzz fiber production.

Claim 17. (Previously Presented) A chimeric gene comprising the following operably linked DNA fragments:

- i) a promoter expressible in plant cells;
- ii) a DNA region coding for a protein comprising the amino acid sequence of SEQ ID No. 6 or a variant thereof having at least 95% amino acid sequence identity to the amino acid sequence of SEQ ID No. 6 and having the same enzymatic activity; and
- iii) a 3'end region involved in transcription termination and polyadenylation.

Claim 18. (Original) The chimeric gene of claim 17, wherein said DNA region comprises the nucleotide sequence of SEQ ID No. 2 or SEQ ID No. 3 or SEQ ID No. 4.

Claim 19. (Original) The chimeric gene of claim 17, wherein said promoter is a constitutive promoter.

Claim 20. (Original) The chimeric gene of claim 17, wherein said promoter is a fiber-specific promoter.

Claim 21. (Original) The chimeric gene of claim 17, wherein said promoter is an expansin promoter.

Claim 22. (Original) A plant cell comprising the chimeric gene of claim 17.

Claim 23. (Original) A plant comprising a plant cell according to claim 22.

Claim 24. (Original) A seed of the plant of claim 23.

Claim 25. (Currently Amended) A chimeric gene comprising
a first nucleotide sequence of at least 21 contiguous nucleotides ~~selected from~~ of a
nucleotide sequence which codes for a protein comprising the amino acid sequence of SEQ
ID No. 6,

operably linked to a plant expressible promoter and a 3' region involved in transcription termination and polyadenylation.

Claim 26. (Original) A chimeric gene according to claim 25, further comprising a second nucleotide sequence complementary to said first nucleotide sequence, operably linked to said first nucleotide sequence such that upon transcription of said chimeric gene, an RNA is formed which can form a double stranded RNA region between said first and said second nucleotide sequence.

Claim 27. (Currently Amended) A chimeric gene according to claim 25, wherein said first sequence of at least 21 contiguous nucleotides is ~~selected~~ from the nucleotide sequence of SEQ ID No. 2.

Claim 28. (Original) A chimeric gene according to claim 27, further comprising a second nucleotide sequence complementary to said first nucleotide sequence, operably linked to said first nucleotide sequence such that upon transcription of said chimeric gene, an RNA is formed which can form a double stranded RNA region between said first and said second nucleotide sequence.

Claim 29. (Original) A plant cell comprising the chimeric gene of claim 25

Claim 30. (Original) A plant comprising a plant cell according to claim 29.

Claim 31. (Original) A seed of the plant of claim 30.

Claim 32. (Currently Amended) A chimeric gene comprising
a first nucleotide sequence of at least 21 contiguous nucleotides ~~selected~~ from the
complement of a nucleotide sequence which codes for a protein comprising the amino acid
sequence of SEQ ID No. 6
operably linked to a plant expressible promoter and a 3' region involved in
transcription termination and polyadenylation.

Claim 33. (Currently Amended) A chimeric gene according to claim 32, wherein said
first nucleotide sequence of at least 21 contiguous nucleotides is ~~selected~~ from the
complement of the nucleotide sequence of SEQ ID No. 2.

Claim 34. (Original) A chimeric gene according to claim 32, wherein said plant
expressible promoter is a constitutive promoter.

Claim 35. (Original) A chimeric gene according to claim 32, wherein said plant
expressible promoter is a fuzz fiber specific promoter.

Claim 36. (Original) A plant cell comprising the chimeric gene of claim 32.

Claim 37. (Original) A plant comprising a plant cell according to claim 36.

Claim 38. (Original) A seed of the plant of claim 37.

Claim 39. (Original) A method for identifying allelic variations of the genes encoding proteins involved in cellulose biosynthesis in a population of different genotypes or varieties of a fiber producing plant species, which are correlated either alone or in combination with the quantity and/or quality of cellulose production, and fiber production comprising the steps of:

- a) providing a population of different varieties or genotypes of a particular plant species or interbreeding plant species comprising different allelic forms of the nucleotide sequences encoding proteins comprising the amino acid sequences of SEQ ID No. 5, 6, 7 or 8;
 - b) determining parameters related to fiber production and/or cellulose biosynthesis or each individual of the population;
 - c) determining the presence of a particular allelic form of the nucleotide sequences encoding proteins comprising the amino acid sequences of SEQ ID No. 5, 6, 7 or 8 for each individual of the population; and
 - d) correlating the occurrence of particular fiber or cellulose parameters with the presence of a particular allelic form of the mentioned nucleotide sequence or a particular combination of such allelic forms;
- and thereby identifying said allelic variations.